

RAW SEQUENCE LISTING

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Application Serial Number: 10/736,892
Source: 1FW0
Date Processed by STIC: 3/15/05

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RAW SEQUENCE LISTING

DATE: 03/15/2005

PATENT APPLICATION: US/10/736,892

TIME: 14:23:18

Input Set : D:\US Utility 50229-424 Sequence Listing.txt

Output Set: N:\CRF4\03152005\J736892.raw

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3 <110> APPLICANT: University of Kentucky Research Foundation
4     JI, Tai
5     JI, Inhae
7 <120> TITLE OF INVENTION: GENES AND AGENTS TO REGULATE FOLLICULAR DEVELOPMENT,
OVULATION
8     CYCLE AND STERIOGENESIS
10 <130> FILE REFERENCE: 050229-0424
12 <140> CURRENT APPLICATION NUMBER: 10/736,892
13 <141> CURRENT FILING DATE: 2003-12-17
15 <150> PRIOR APPLICATION NUMBER: 60/437,729
16 <151> PRIOR FILING DATE: 2003-01-03
18 <160> NUMBER OF SEQ ID NOS: 13
20 <170> SOFTWARE: PatentIn version 3.3
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 21
24 <212> TYPE: DNA
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: Chemically synthesized
30 <400> SEQUENCE: 1
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35 <211> LENGTH: 21
36 <212> TYPE: DNA
37 <213> ORGANISM: Artificial Sequence
39 <220> FEATURE:
40 <223> OTHER INFORMATION: Chemically synthesized
42 <400> SEQUENCE: 2
43 acagtatgca ggcttcgctc c                                21
46 <210> SEQ ID NO: 3
47 <211> LENGTH: 21
48 <212> TYPE: DNA
49 <213> ORGANISM: Artificial Sequence
51 <220> FEATURE:
52 <223> OTHER INFORMATION: Chemically synthesized
54 <400> SEQUENCE: 3
55 gctttccctc tgttgaccca c                                21
58 <210> SEQ ID NO: 4
59 <211> LENGTH: 21
60 <212> TYPE: DNA
61 <213> ORGANISM: Artificial Sequence
63 <220> FEATURE:
64 <223> OTHER INFORMATION: Chemically synthesized
66 <400> SEQUENCE: 4

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70 <210> SEQ ID NO: 5
71 <211> LENGTH: 21
72 <212> TYPE: DNA
73 <213> ORGANISM: Artificial Sequence
75 <220> FEATURE:
76 <223> OTHER INFORMATION: Chemically synthesized
78 <400> SEQUENCE: 5
79 ctgaaggtca aagggaaatgt g 21
82 <210> SEQ ID NO: 6
83 <211> LENGTH: 21
84 <212> TYPE: DNA
85 <213> ORGANISM: Artificial Sequence
87 <220> FEATURE:
88 <223> OTHER INFORMATION: Chemically synthesized
90 <400> SEQUENCE: 6
91 ggacagagtc ttgatgatct c 21
94 <210> SEQ ID NO: 7
95 <211> LENGTH: 1099
96 <212> TYPE: DNA
97 <213> ORGANISM: Rattus norvegicus
99 <400> SEQUENCE: 7
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102 tccgcagctc cagcctcctc atcccgcccc tggaggccgc actggccaac ttctccaaag 120
104 gtcccgcagg aggggtcatg caaccgggtgc gcaccgtggt gcctgtggcc aagcaccgag 180
106 gcttcttggg agtcatgcca gcctacagtgc ccgctgagga tgcaactcacc accaagttag 240
108 tcaccttcta tgagggccac agcaacaatg ctgtcccctc ccaccaggca tcagtgtctc 300
110 tctttgatcc cagcaatggt tccctgctgg cggtcatgga tggaaatgtc ataactgcaa 360
112 agaggacagc agccgtctct gccatcgcca ccaagttttt gaagccccca ggcagtgatg 420
114 tgctgtgcat tcttggggct ggggtccagg cgtacagtca ctatgagatc ttcacagaac 480
116 agttctcctt caaggagggtg agaatgtgga accgcaccag ggaaaatgct gagaagtttg 540
118 caagctcagt gcaggagatg gttcgggtct gtccatcagt gcaggaggct gtgacagggtg 600
120 ccgatgtcat catcacagtc accatggcaa cggagcccat tttatttggt gaatgggtga 660
122 agcccggggc tcacatcaat gctgttggag ccagtagacc tgactggcga gaactggatg 720
124 acgagctcat gaagcaagca gtgctgtatg tggactcccc ggaggctgcc ctaaaggagt 780
126 caggagatgt tctgttgtca ggggctgaca tctttgctga gcttggagaa gtggtttcag 840
128 gagcgaagcc tgcatactgt gagaagacca cgggtgttcaa gtctttgggg atggcagtgg 900
130 aggacctggt cgcagccaaa ttagtgtacg attcgtggtc atctggcaag tgagcagaag 960
132 gagctgtgcc tgggctggat ggacgtcacg gctcaaacgc tggctcagtg tctagatcaa 1020
134 aggaggccta gtccccagtg aacgggagtg agagtcactc ataagtattg acatccctat 1080
136 tcatgtttgt ggttggata 1099
139 <210> SEQ ID NO: 8
140 <211> LENGTH: 313
141 <212> TYPE: PRT
142 <213> ORGANISM: Rattus norvegicus
144 <400> SEQUENCE: 8
146 Met Arg Arg Ala Pro Ala Phe Leu Ser Ala Asp Glu Val Gln Asp His
147 1 5 10 15
150 Leu Arg Ser Ser Ser Leu Leu Ile Pro Pro Leu Glu Ala Ala Leu Ala

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151          20          25          30
154 Asn Phe Ser Lys Gly Pro Asp Gly Gly Val Met Gln Pro Val Arg Thr
155          35          40          45
158 Val Val Pro Val Ala Lys His Arg Gly Phe Leu Gly Val Met Pro Ala
159          50          55          60
162 Tyr Ser Ala Ala Glu Asp Ala Leu Thr Thr Lys Leu Val Thr Phe Tyr
163 65          70          75          80
166 Glu Gly His Ser Asn Asn Ala Val Pro Ser His Gln Ala Ser Val Leu
167          85          90          95
170 Leu Phe Asp Pro Ser Asn Gly Ser Leu Leu Ala Val Met Asp Gly Asn
171          100         105         110
174 Val Ile Thr Ala Lys Arg Thr Ala Ala Val Ser Ala Ile Ala Thr Lys
175          115         120         125
178 Phe Leu Lys Pro Pro Gly Ser Asp Val Leu Cys Ile Leu Gly Ala Gly
179          130         135         140
182 Val Gln Ala Tyr Ser His Tyr Glu Ile Phe Thr Glu Gln Phe Ser Phe
183 145         150         155         160
186 Lys Glu Val Arg Met Trp Asn Arg Thr Arg Glu Asn Ala Glu Lys Phe
187          165         170         175
190 Ala Ser Ser Val Gln Gly Asp Val Arg Val Cys Ser Ser Val Gln Glu
191          180         185         190
194 Ala Val Thr Gly Ala Asp Val Ile Ile Thr Val Thr Met Ala Thr Glu
195          195         200         205
198 Pro Ile Leu Phe Gly Glu Trp Val Lys Pro Gly Ala His Ile Asn Ala
199          210         215         220
202 Val Gly Ala Ser Arg Pro Asp Trp Arg Glu Leu Asp Asp Glu Leu Met
203 225         230         235         240
206 Lys Gln Ala Val Leu Tyr Val Asp Ser Arg Glu Ala Ala Leu Lys Glu
207          245         250         255
210 Ser Gly Asp Val Leu Leu Ser Gly Ala Asp Ile Phe Ala Glu Leu Gly
211          260         265         270
214 Glu Val Val Ser Gly Ala Lys Pro Ala Tyr Cys Glu Lys Thr Thr Val
215          275         280         285
218 Phe Lys Ser Leu Gly Met Ala Val Glu Asp Leu Val Ala Ala Lys Leu
219          290         295         300
222 Val Tyr Asp Ser Trp Ser Ser Gly Lys
223 305         310
226 <212> SEQ ID NO: 9
227 <212> LENGTH: 313
228 <212> TYPE: PRT
229 <213> ORGANISM: Mus musculus
231 <400> SEQUENCE: 9
233 Met Lys Arg Ala Pro Ala Phe Leu Ser Ala Glu Glu Val Gln Asp His
234 1          5          10          15
237 Leu Arg Ser Ser Ser Leu Leu Ile Pro Pro Leu Glu Ala Ala Leu Ala
238          20          25          30
241 Asn Phe Ser Lys Gly Pro Asp Gly Gly Val Met Gln Pro Val Arg Thr
242          35          40          45
245 Val Val Pro Val Ala Lys His Arg Gly Phe Leu Gly Val Met Pro Ala

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246      50      55      60
249 Tyr Ser Ala Ala Glu Asp Ala Leu Thr Thr Lys Leu Val Thr Phe Tyr
250 65      70      75      80
253 Glu Gly His Ser Asn Thr Ala Val Pro Ser His Gln Ala Ser Val Leu
254      85      90      95
257 Leu Phe Asp Pro Ser Asn Gly Ser Leu Leu Ala Val Met Asp Gly Asn
258      100      105      110
261 Val Ile Thr Ala Lys Arg Thr Ala Ala Val Ser Ala Ile Ala Thr Lys
262      115      120      125
265 Leu Leu Lys Pro Pro Gly Ser Asp Val Leu Cys Ile Leu Gly Ala Gly
266      130      135      140
269 Val Gln Ala Tyr Ser His Tyr Glu Ile Phe Thr Glu Gln Phe Ser Phe
270 145      150      155      160
273 Lys Glu Val Arg Met Trp Asn Arg Thr Arg Glu Asn Ala Glu Lys Phe
274      165      170      175
277 Ala Ser Thr Val Gln Gly Asp Val Arg Val Cys Ser Ser Val Gln Glu
278      180      185      190
281 Ala Val Thr Gly Ala Asp Val Ile Ile Thr Val Thr Met Ala Thr Glu
282      195      200      205
285 Pro Ile Leu Phe Gly Glu Trp Val Lys Pro Gly Ala His Ile Asn Ala
286      210      215      220
289 Val Gly Ala Ser Arg Pro Asp Trp Arg Glu Leu Asp Asp Glu Leu Met
290 225      230      235      240
293 Arg Gln Ala Val Leu Tyr Val Asp Ser Arg Glu Ala Ala Leu Lys Glu
294      245      250      255
297 Ser Gly Asp Val Leu Leu Ser Gly Ala Asp Ile Phe Ala Glu Leu Gly
298      260      265      270
301 Glu Val Ile Ser Gly Ala Lys Pro Ala His Cys Glu Lys Thr Thr Val
302      275      280      285
305 Phe Lys Ser Leu Gly Met Ala Val Glu Asp Leu Val Ala Ala Lys Leu
306      290      295      300
309 Val Tyr Asp Ser Trp Ser Ser Gly Lys
310 305      310
313 <210> SEQ ID NO: 10
314 <211> LENGTH: 314
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <400> SEQUENCE: 10
320 Met Ser Arg Val Pro Ala Phe Leu Ser Ala Ala Glu Glu Glu Asp His
321 1      5      10      15
324 Leu Arg Ser Ser Ser Leu Leu Ile Pro Pro Leu Glu Thr Ala Leu Ala
325      20      25      30
328 Asn Phe Ser Ser Gly Glu Asp Gly Gly Val Met Gln Pro Val Arg Thr
329      35      40      45
332 Val Val Pro Val Thr Lys His Arg Gly Tyr Leu Gly Val Met Pro Ala
333      50      55      60
336 Tyr Ser Ala Ala Glu Asp Ala Leu Thr Thr Lys Leu Val Thr Phe Tyr
337 65      70      75      80
340 Glu Asp Arg Gly Ile Thr Ser Val Val Pro Ser His Gln Ala Thr Val

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341          85          90          95
344 Leu Leu Phe Glu Pro Ser Asn Gly Thr Leu Leu Ala Val Met Asp Gly
345          100          105          110
348 Asn Val Ile Thr Ala Lys Arg Thr Ala Ala Val Ser Ala Ile Ala Thr
349          115          120          125
352 Lys Phe Leu Lys Pro Pro Ser Ser Glu Val Leu Cys Ile Leu Gly Ala
353          130          135          140
356 Gly Val Gln Ala Tyr Ser His Tyr Glu Ile Phe Thr Glu Gln Phe Ser
357 145          150          155          160
360 Phe Lys Glu Val Arg Ile Trp Asn Arg Thr Lys Glu Asn Ala Glu Lys
361          165          170          175
364 Phe Ala Asp Thr Val Gln Gly Glu Val Arg Val Cys Ser Ser Val Gln
365          180          185          190
368 Glu Ala Val Ala Gly Ala Asp Val Ile Ile Thr Val Thr Leu Ala Thr
369          195          200          205
372 Glu Pro Ile Leu Phe Gly Glu Trp Val Lys Pro Gly Ala His Ile Asn
373          210          215          220
376 Ala Val Gly Ala Ser Arg Pro Asp Trp Arg Glu Leu Asp Asp Glu Leu
377 225          230          235          240
380 Met Glu Gln Ala Val Leu Tyr Val Asp Ser Gln Glu Ala Ala Leu Lys
381          245          250          255
384 Glu Ser Gly Asp Val Leu Leu Ser Gly Ala Glu Ile Phe Ala Glu Leu
385          260          265          270
388 Gly Glu Val Ile Lys Gly Val Lys Pro Ala His Cys Glu Lys Thr Thr
389          275          280          285
392 Val Phe Lys Ser Leu Gly Met Ala Val Glu Asp Thr Val Ala Ala Lys
393          290          295          300
396 Leu Ile Tyr Asp Ser Trp Ser Ser Gly Lys
397 305          310

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400 <210> SEQ ID NO: 11

401 <211> LENGTH: 1015

402 <212> TYPE: DNA

403 <213> ORGANISM: Rattus norvegicus

405 <400> SEQUENCE: 11

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408 gagatttctg aaagaaaact gccgtccaga tggaagagaa cttggtgaat tcagaaccac      120
410 aactgtcaac ataggttcga tcagtacagc ggatggctct gctctagtga agctggggaa      180
412 caccacagtc atttgtggag ttaaagcaga atttgcagca ccaccagtag atgcccctga      240
414 tagaggatat gtcgtcccta atgtggacct accaccgctg tgttcatcga ggtttcggac      300
416 tggacctcct ggagaagagg ctcaagtaac cagccagttc attgcagatg tcattgagaa      360
418 ctcacacata attaagaaag aggacttatg catttctcca gggaaagcttg cttgggttct      420
420 atactgtgac cttatttgcc tagactacga tgggaaacatt ttggatgcct gcacatttgc      480
422 tttgttagca gctttaaaga atgtacagtt gcctgaagtt actataaatg aagaaaactgc      540
424 tttagcggaa gtcaatttaa agaagaaaag ttatttgaat gttagagcaa acccagttgc      600
426 tacttcattt gctgtgtttg atgacacttt gctgatagtc gatcctaccg gggaggaggg      660
428 gcacctgtc cacaggaacc ttaaccgtag taatggacga ggaaggcaag ctgtgctgtc      720
430 ttcacaagcc aggtgggagt gggctgctgg agctaaactt caggactgca tgagtcgagc      780
432 agtaacgaga cacaaagaag tgagcaaaact actggatgaa gtaattcaga gcatgaaaca      840
434 caaatgaaca gacgccacga ttgtaaaaca gctgtaaaaa ttgtatttgt tacactgtgc      900

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VERIFICATION SUMMARY

DATE: 03/15/2005

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